

**Primary structure of human nonmuscle-type cofilin**  
**(AC: P23528)**

MASGVAVSDG VIKVFNDMKV RKSSTPEEVK KRKKAVLFCL SEDKKNIILE  
EGKEILVGDV

GQTVDDPYAT FVKMLPDKDC RYALYDATYE TKESKKEDLV FIFWAPESAP  
LKSKMIYASS

KDAIKKKLTG IKHELQANCY EEVKDRCTLA EKLGGSAVIS LEGKPL

The underlined portions are the sites analyzed for  
sequence by MS and MS/MS.

Met Ala Ser Gly Val Ala Val Ser Asp Gly Val Ile Lys Val Phe Asn

5 10 15

Asp Met Lys Val Arg Lys Ser Ser Thr Pro Glu Glu Val Lys Lys Arg

20 25 30

Lys Lys Ala Val Leu Phe Cys Leu Ser Glu Asp Lys Lys Asn Ile Ile

35 40 45

Leu Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Gln Thr Val

50 55 60

Asp Asp Pro Tyr Ala Thr Phe Val Lys Met Leu Pro Asp Lys Asp Cys

65 70 75 80

Arg Tyr Ala Leu Tyr Asp Ala Thr Tyr Glu Thr Lys Glu Ser Lys Lys

85 90 95

Glu Asp Leu Val Phe Ile Phe Trp Ala Pro Glu Ser Ala Pro Leu Lys

100 105 110

Ser Lys Met Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Leu

115 120 125

Thr Gly Ile Lys His Glu Leu Gln Ala Asn Cys Tyr Glu Glu Val Lys

130 135 140

Asp Arg Cys Thr Leu Ala Glu Lys Leu Gly Gly Ser Ala Val Ile Ser

145 150 155 160

Leu Glu Gly Lys Pro Leu

165

**Fig. 1**

**cDNA of human placental nonmuscle-type cofilin**  
**(AC: D00682)**

atggcctccg gtgtggctgt ctctgatggt gtcataagg tgttcaacga catgaaggtg 60  
cgtaagtctt caacgccaga ggaggtgaag aagcgcaaga aggcggtgct cttctgcctg 120  
agtgaggaca agaagaacat catcctggag gagggaagg agatcctggt gggcgatgtg 180  
ggccagactg tcgacgatcc ctacgccacc ttgtcaaga tgctgccaga taaggactgc 240  
cgctatgccc tctatgatgc aacctatgag accaaggaga gcaagaagga ggatctggtg 300  
tttatcttct gggcccccca gtctgcgccc cttaagagca aaatgattta tgccagctcc 360  
aaggacgcca tcaagaagaa gctgacaggg atcaagcatg aattgcaagc aaactgctac 420  
gaggaggcca aggaccgctg caccctggca gagaagctgg ggggcagtgc ggtcatctcc 480  
ctggaggcca agcctttgtg a 501

The underlined portions are the sites where two  
oligomers were synthesized as primers.

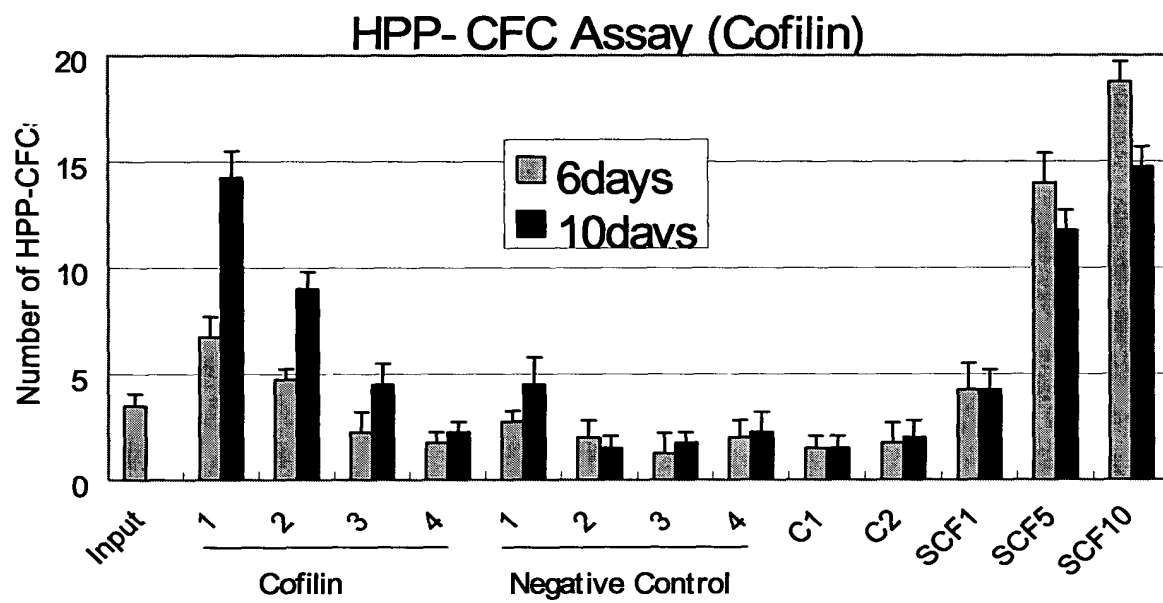
**Fig. 2**

**Alignment of the base sequences for nonmuscle-type cofilin  
derived from human placenta (upper)  
and from human S6 cells (lower).**

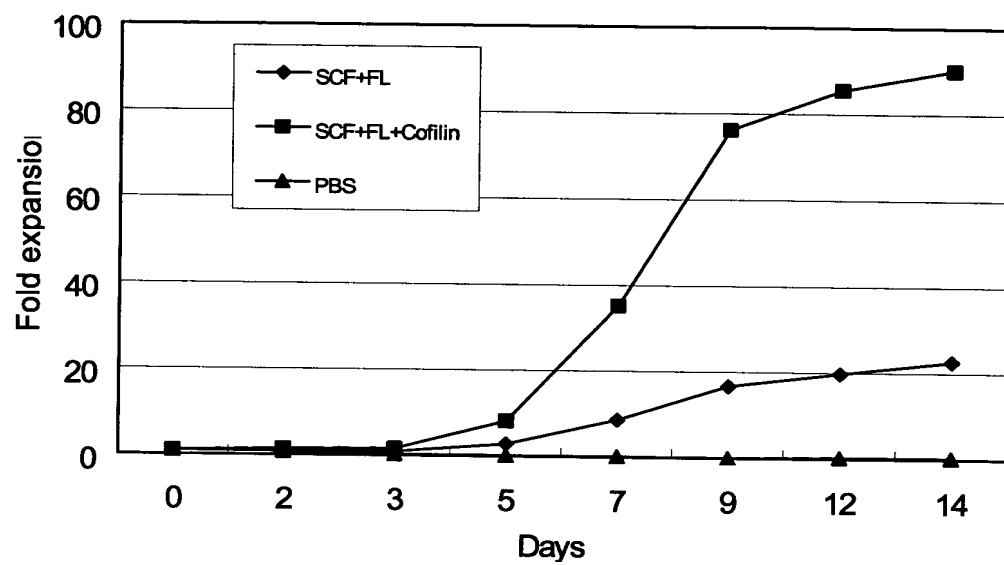
		10	20	30	40	50
Placental cDNA	1	ATGGCCTCCG	GTGTGGCTGT	CTCTGATGGT	GTCATCAAGG	
TGTTCAACGA	50					
S6 cDNA		1	ATGGCCTCCG	GTGTGGCTGT	CTCTGATGGT	GTCATCAAGG
TGTTCAACGA	50					
		60	70	80	90	100
Placental cDNA	51	CATGAAGGTG	CGTAAGTCTT	CAACGCCAGA	GGAGGTGAAG	
AAGCGCAAGA	100					
S6 cDNA		51	CATGAAGGTG	CGTAAGTCTT	CAACGCCAGA	
GGAGGTGAAG	AAGCGCAAGA	100				
		110	120	130	140	150
Placental cDNA	101	AGGCGGTGCT	CTTCTGCCTG	AGTGAGGACA	AGAAGAACAT	
CATCCTGGAG	150					
S6 cDNA		101	AGGCGGTGCT	CTTCTGCCTG	AGTGAGGACA	
AGAAGAACAT	CATCCTGGAG	150				
		160	170	180	190	200
Placental cDNA	151	GAGGGCAAGG	AGATCCTGGT	GGGCGATGTG	GGCCAGACTG	
TCGACGATCC	200					
S6 cDNA		151	GAGGGCAAGG	AGATCCTGGT	GGGCGATGTG	
GGCCAGACTG	TCGACGATCC	200				
		210	220	230	240	250
Placental cDNA	201	CTACGCCACC	TTTGTCAAGA	TGCTGCCAGA	TAAGGACTGC	
CGCTATGCCC	250					
S6 cDNA		201	CTACGCCACC	TTTGTCAAGA	TGCTGCCAGA	TAAGGACTGC
CGCTATGCCC	250					
		260	270	280	290	300
Placental cDNA	251	TCTATGATGC	AACCTATGAG	ACCAAGGAGA	GCAAGAAGGA	
GGATCTGGTG	300					
S6 cDNA		251	TCTATGATGC	AACCTATGAG	ACCAAGGAGA	
GCAAGAAGGA	GGATCTGGTG	300				
		310	320	330	340	350
Placental cDNA	301	TTTATCTTCT	GGGCCCCCGA	GTCTGCGCCC	CTTAAGAGCA	
AAATGATTTA	350					
S6 cDNA		301	TTTATCTTCT	GGGCCCCCGA	GTCTGCGCCC	CTTAAGAGCA
AAATGATTTA	350					
		360	370	380	390	400
Placental cDNA	351	TGCCAGCTCC	AAGGACGCCA	TCAAGAAGAA	GCTGACAGGG	
ATCAAGCATG	400					
S6 cDNA		351	TGCCAGCTCC	AAGGACGCCA	TCAAGAAGAA	
GCTGACAGGG	ATCAAGCATG	400				
		410	420	430	440	450
Placental cDNA	401	AATTGCAAGC	AAACTGCTAC	GAGGAGGTCA	AGGACCGCTG	
CACCCTGGCA	450					
S6 cDNA		401	AATTGCAAGC	AAACTGCTAC	GAGGAGGTCA	
AGGACCGCTG	CACCCTGGCA	450				
		460	470	480	490	500
Placental cDNA	451	GAGAAGCTGG	GGGGCAGTGC	GGTCATCTCC	CTGGAGGGCA	
AGCCTTTGTG	500					
S6 cDNA		451	GAGAAGCTGG	GGGGCAGTGC	CGTCATCTCC	
CTGGAGGGCA	AGCCTTTGTG	500				
		510	520	530	540	550
Placental cDNA	501	A.....	.....	.....	.....	.....
S6 cDNA		501	A.....	.....	.....	.....

The two bases that differ between the two sequences are marked by shadowing and are both due to silent mutation.

**Fig. 3**

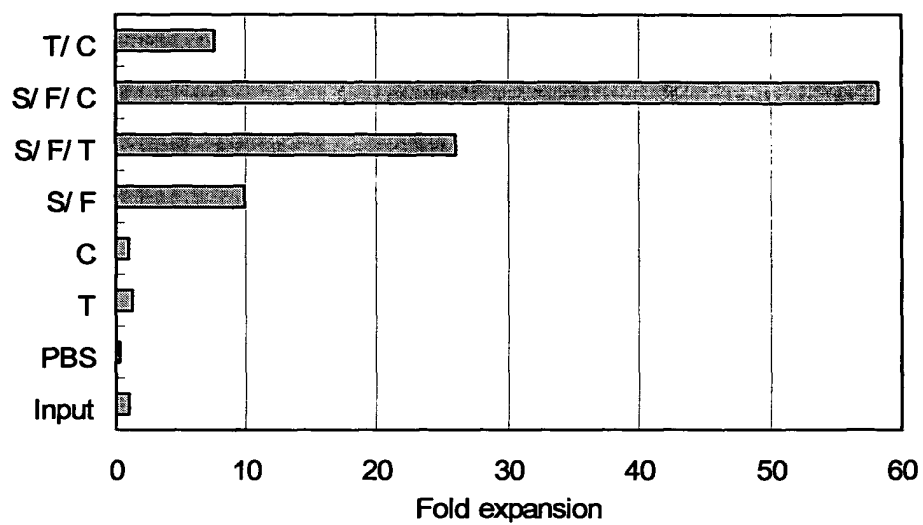


**Fig. 4**

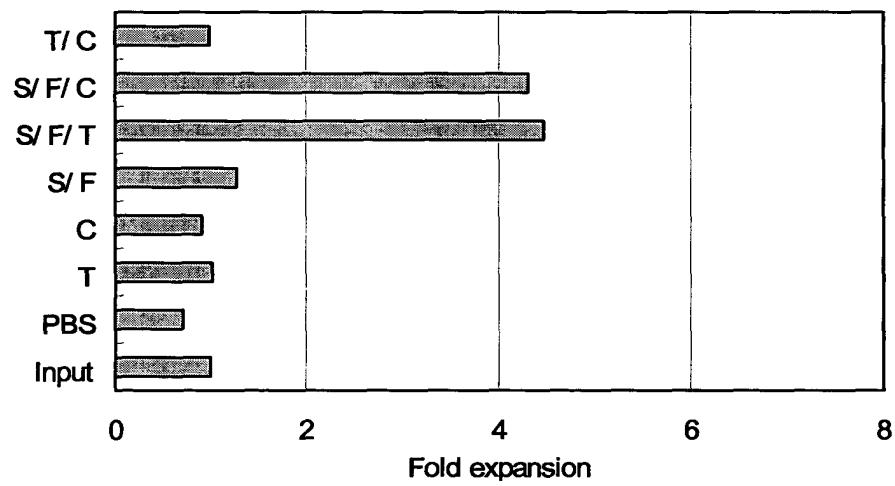


**Fig. 5**

**A**

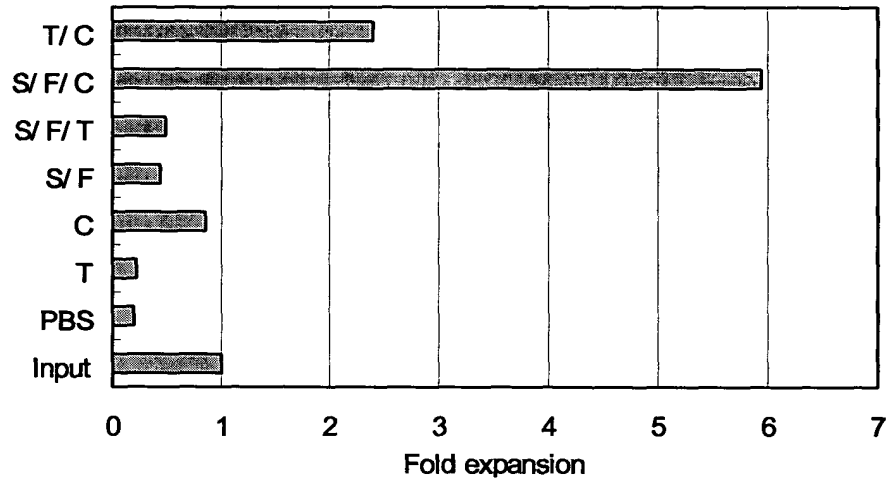


**B**



**Fig. 6**

C



D

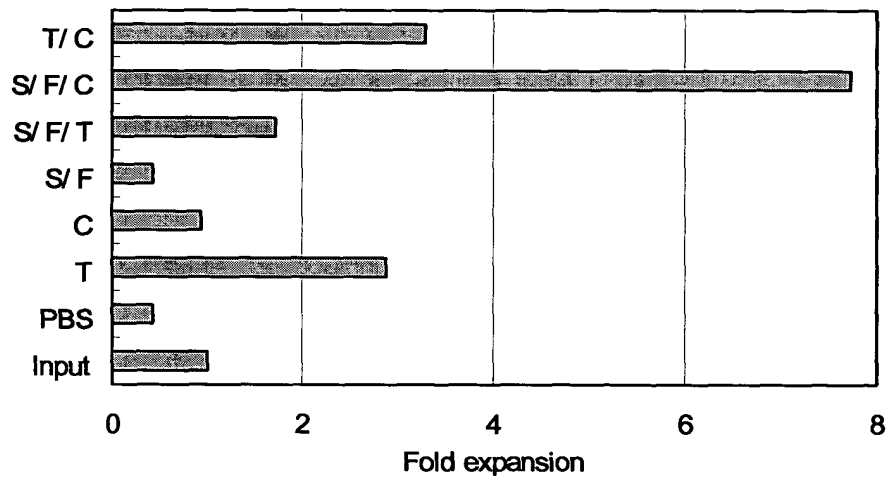
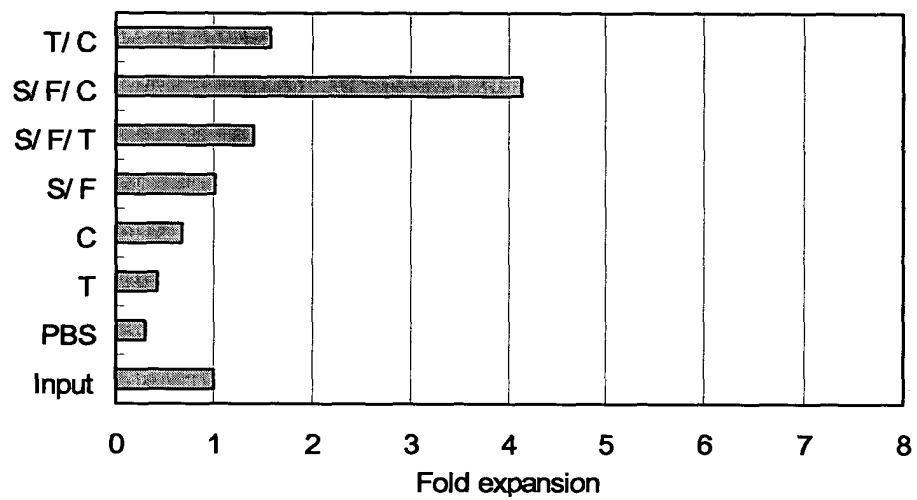
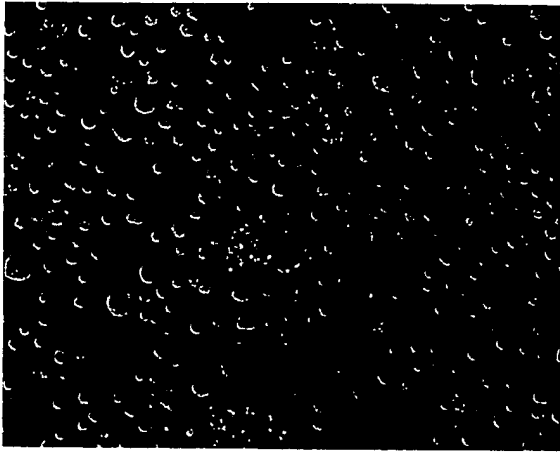


Fig. 6 (Cont.)



**Fig. 7**





**Fig. 8**



Fig. 9